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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:21:43 ; Search time 90 Seconds

(without alignments)
8430.418 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccgaatttga.....aaatctcgttataaaaatt 1719

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCrUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	295.8	17.2	1566	4. US-09-328-352-1297	Sequence 1297, Ap
2	284.8	16.6	580073	4. US-08-545-528D-1	Sequence 1, Appli
3	271.2	15.8	1554	4. US-09-134-001C-2607	Sequence 2607, Ap
4	153.2	8.9	1557	4. US-09-252-991A-6920	Sequence 6920, Ap
5	153.2	8.9	1590	4. US-09-252-991A-6824	Sequence 6824, Ap
6	105.4	6.1	741	4. US-09-252-991A-6774	Sequence 6774, Ap
7	95.2	5.5	2094	3. US-08-714-918-87	Sequence 87, Appl
8	95.2	5.5	2094	3. US-09-265-315-87	Sequence 87, Appl
9	95.2	5.5	2094	3. US-09-265-315-87	Sequence 87, Appl
10	95.2	5.5	2094	3. US-09-266-417-87	Sequence 87, Appl
11	81.4	4.7	484	3. US-08-975-762-34	Sequence 34, Appl
12	81.4	4.7	484	3. US-08-821-324-34	Sequence 34, Appl
13	81.4	4.7	484	3. US-09-295-028-34	Sequence 34, Appl
14	81.4	4.7	484	3. US-09-106-582-34	Sequence 34, Appl
15	39.8	2.3	2861	4. US-09-398-395A-55	Sequence 55, Appl
16	39.8	2.3	2861	4. US-09-887-586A-55	Sequence 55, Appl
17	39.8	2.3	2861	4. US-09-895-752-55	Sequence 55, Appl
18	39.8	2.3	2861	4. US-09-903-012B-55	Sequence 55, Appl
19	37.8	2.2	521	4. US-09-669-751-138	Sequence 138, App
20	37.8	2.2	864	4. US-09-601-198-85	Sequence 85, Appl
21	37.4	2.2	1329	4. US-09-134-001C-196	Sequence 196, App
22	36.6	2.1	3095	6. 5231168-1	Patent No. 5231168
23	36.4	2.1	1557	4. US-09-134-001C-1614	Sequence 1614, Ap
24	36.2	2.1	319608	4. US-09-679-409-1	Sequence 1, Appli
25	36.2	2.1	1664976	4. US-08-916-421B-1	Sequence 1, Appli
26	36.2	2.1	1664976	4. US-08-916-421B-1	Sequence 1, Appli
27	36	2.1	729	3. US-08-998-416-1031	Sequence 1031, Ap

28	35.8	2.1	319608	4	US-09-539-333D-1	Sequence 1, Appli
29	35.6	2.1	2088	4	US-09-328-352-624	Sequence 624, App
30	35.4	2.1	648	4	US-09-328-352-2915	Sequence 2915, Ap
31	35.4	2.1	6027	2	US-08-968-542C-1	Sequence 1, Appli
32	35.4	2.1	6216	3	US-09-213-053-1	Sequence 1, Appli
33	35.2	2.0	2355	4	US-08-913-159-12	Sequence 12, Appli
34	35.2	2.0	29793	4	US-09-302-812-38	Sequence 38, Appli
35	35.2	2.0	29793	4	US-09-511-477-38	Sequence 38, Appli
36	35.2	2.0	29793	4	US-09-511-507-38	Sequence 38, Appli
37	34.8	2.0	1200	4	US-09-328-352-3506	Sequence 3506, Ap
38	34.8	2.0	1311	3	US-08-584-760A-66	Sequence 66, Appli
39	34.6	2.0	12286	4	US-09-322-478-17	Sequence 17, Appli
40	34.6	2.0	12571	4	US-09-322-478-20	Sequence 20, Appli
41	34.4	2.0	366	4	US-09-134-001C-2003	Sequence 2003, Ap
42	34.4	2.0	1380	4	US-09-134-001C-2019	Sequence 2019, Ap
43	34.4	2.0	4383	6	5175095-4	Patent No. 5175095
44	34.4	2.0	580073	4	US-08-545-528D-1	Sequence 1, Appli
45	34.2	2.0	1446	4	US-09-601-198-140	Sequence 140, App

ALIGNMENTS

RESULT 1

US-09-328-352-1297

; Sequence 1297, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/328.352

; CURRENT FILING DATE: 1998-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 1297

; LENGTH: 1566

; TYPE: DNA

; ORGANISM: Acinetobacter baumannii

US-09-328-352-1297

Query Match 17.2%; Score 295.8; DB 4; Length 1566;
Best Local Similarity 55.4%; Pred. No. 8.3e-72;
Matches 702; Conservative 0; Mismatches 547; Indels 18; Gaps 6;

Qy	178	GGTCTTCATGTTGATGTCAGAGGCTTATGGAATCTGAATGGACATTTGAAT	237
Db	178	GGTGAAGATGTTGTTTACCTGATGGACAAATGGTAACCTCGGAAGTTGGTCACATGAAC	237
Qy	238	ATAGCAGCTGGAAGATTTATTTCAAGATATTCTGGAATTAATTTGGCTGTTCACGCA	297
Db	238	CTTGCGCTGCCGAGTGTATACCAAGACTTCACACGTATTACTAAAGATATTCGTACT	297
Qy	298	AACGAGTTTGTACAAATCTCAGATTGTTGCATCAGTCAGTCGCAAGAGGGGAGT	357
Db	298	GGTCTTTTGTAGCAGCAAGATATTGTTGATCCGTAGAAAAAGCAAGACGCGGT	357
Qy	358	GGTCGATGATTTATTAGGACTGGTTAGCCATGGTGGTCCACTCTCATATTGATCAT	417
Db	358	GGTCGATGATTTATTAGGACTGGTTAGCCATGGTGGTCCACTCTCATATTGATCAT	417
Qy	418	CTTTTTCGTTGATGATGCTGATTTAAACAATTAACAAGTGCCAAAGGTTTTTCATTCAC	477
Db	418	ATTGTGGC---GATGTGTGACTTTGCCTTAAACCGCGGTGCGAAGTTTACTTACATGCA	474
Qy	478	TTTGCTGATGTCGAGATACCTTCGCCAACAAAGTGGAGCTGGTTATCTTGAACAACTTCT	537
Db	475	TTCTTGTATGTCGTCGACACTCCCTCCAGTAGTGTCTCAACCTTCATTAGAAAAATAGAC	534
Qy	538	CAATTTATGCT---TCGGAAGAGTACGGAGAAATGGCTACTATTAAGTGGACGTTATAT	594
Db	535	GCATTATTCGCTAAATATCCGAACCAAGGCGGTATTGCAACCATGATTTGGTGGCTATTTT	594

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6824
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6824

Query Match 8.9%; Score 153.2; DB 4; Length 1590;
Best Local Similarity 47.9%; Pred. No. 1.6e-32;
Matches 582; Conservative 0; Mismatches 613; Indels 21; Gaps 4;

QY 177 CGGTCTTCATGTTGGATTGCCAGAGGCTTAATGGGAAATTCGAAGTTGGAGATTGAA 236
DB 192 CGGCATGGAGCTGGGCTGCCGACGCCAGATGGCAATTCCGAGGTCCGCCACATGAA 251
QY 237 TATAGGAGCTGGAAGAGTATTATCAAGATATTGTTGGAATTAATTTGGCTGTCAACG 296
DB 252 CCTCGCGGAGCGCGGTGTGTACAGGACTTACCCCGCGTCAACAGGCCATCCCGCA 311
QY 297 AAACGAGTTTGTACAAATCCTCAGATTTGTGCATCAGCTGAGCGTCAAGAGGGAG 356
DB 312 CGCGGAATTTCTGAAACCCGGTGTATCGCGCGGGTGCAGCAAGSCGCTCGCGCGCA 371
QY 357 TGGTCGATTCATATTATAGGACTGGTTAGCGATGGTGGTGCACACTCTCATATTGATCA 416
DB 372 CAAGCGGTGCATCCTCGGCTGTCTCCCGCGCGGTATACAGCCATGAAGACCA 431
QY 417 TCTTTTTCGCTGATAGCTGCAATTTAAACAATTAAGTCCCAAGGTTTTCATTCATT 476
DB 432 CTGTGGCAATGCGCGAGATGCGGCCAAGCGCGCGCGGCAAGATCTACTTCATGC 491
QY 477 TTTTGTGTGGTTCGAGATACTTCGCCAACAAGTGGAGCTGGTATCTTGAACAACATCT 536
DB 492 CTCTCTGATGGCGCGCATACCCCGCGGAAAGCGCGAGCGTCTGCGTGGAGCGTCTCGA 551
QY 537 TCAATTTATTTCTCGGAAAGTACGGAGAAATTTGGCTACTATTACTGGAGCTTATTATGC 596
DB 552 CGCCACCTTCGCGCGGCTCGGCAAGGCGCGCATCGCTCGATCATCGGCGCTATTTCGC 611
QY 597 AATGATAGGACAAAAGATGGAGCGTATTAAAGTATGAGGCAATTTATGAGGCAATTTG 656
DB 612 GATGGACCGGACACCGCTGGACCGCGTCCAGCGCGCTATGAAGTATGTCGACGG 671
QY 657 TATTGGACAAAAGCCACCGCTTGATAGGCTGTCGATGTTGTTAGAGAGCGATATGCTCA 716
DB 672 CAAGGCGCGAGTT---CACCGCGGACTCTCGGTGGCAGCCCTCGAGSCCGCTAGCGCCG 728
QY 717 ATCTGAGACTGACGAATTTCTGAACCAATTTT---CGGACGATGG 764
DB 729 CGCGGAGAGGCGCAATTTCTGAAGGCCACCGCGGTGTCGCCGCGCGCGCGCAAGCGGT 788
QY 765 GCGAGTAAAGATGACCATCTCTATTCTTCAATTAATTCGTGCTGATGCTATGCTGCTCA 824
DB 789 GCGGTCGAGATGGCGACCGGCTGATCTTCATGAATTCGCGCGCGCGCGCGCGCGCA 848
QY 825 AATTGTGAATGTTGGGTCTCGAAGCTTTAAAGATCTTTAATGTTTCGTTTCTCTACCC 884
DB 849 GCTGAGCGCGCGCTTCG---TCGAGCGGCGATTAATGAGTTCCTCCCGCGCAAGCGCC 905
QY 885 TAAATAATTCAGATGAGTGGATGACCAATCAATAAGAGTTTCCATTTCATTCGTT 944
DB 906 GCAGCTGGCAGGTTTCTGATGTCGACCCAGTACGCGCGGAGCATCCCGCGCGCTCGC 965
QY 945 ATTCCCACTGTGACTCATACTAATGCTGCTGTAATGCTGCTTCTCTCAAGAGTTAC 1004
DB 966 CTTCGCCCGGAGCGCTGACCAACGTCCTCGCGGAGTACTTGGCCCAAGCATGCGAAGC 1025
QY 1005 TCAATTTCACTGTGCGGAACTGAGAAATGATCTCTCATGTTTACCTTCTTCTTAATGTTG 1064

DB 1026 CCAGCTGGCGCATCGCGGAGACCCGAGAAGTACGCCCATGTGACCTTCTTCTCCGCGG 1085
QY 1065 TCGAGAAGTTCAATTCAGATGAAGAGCGTTGTATGGTTCCTGTCACCAAGAAAGTTGC 1124
DB 1086 CCGCGAGGAACCTCTAGGAGGCGGAGGAGCATCTGATCCCTCCGCGCA---AGGTGCG 1142
QY 1125 TACATATGATTTAAACACGAAATGAATGCTGCTGGAGTTGCCGAAAAAATGTCGAGCA 1184
DB 1143 CACCTAGGACCTGCACCCGAGATAGCGCGCGGGAAGTACCAGACGCTATGCTCGAGGC 1202
QY 1185 AATTGAGTACAGGAGGCATCCTTTTGGTTATGTGCAATTTTTCGCGCTCTTGACATGTTGG 1244
DB 1203 CATCGAGCAACACGCGCTACGACGTGATCGTGGTCAACTACGCCAACGCGACATGGTCGG 1262
QY 1245 ACATAGTGGTAAATTTGAACCTGCCGTCAAGCATGTCAAGCTACTGACGAGGCAATGG 1304
DB 1263 CCACCGGGGTGTTGAGGCGCGGTCTAGGCGCGTCTAGGCGGTGAGTGGCTTGACACCTG 1322
QY 1305 AAAGATATTTGAAGCATGCCAACTTATAATTAAGTTTCTTATGGTTACTTCCGATCATGG 1364
DB 1323 CCGTATCTCGAGCGCTGCACAGGTGCGGCGGAAGCCTGATCATCCGCGGACCAAG 1382
QY 1365 AATGCTGAGAAGATG 1380
DB 1383 CAATGTCGAGCAGATG 1398

RESULT 6

US-09-252-991A-6774
; Sequence 6774, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6774
; LENGTH: 741
; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6774

Query Match 6.1%; Score 105.4; DB 4; Length 741;
Best Local Similarity 52.5%; Pred. No. 1.7e-19;
Matches 279; Conservative 0; Mismatches 246; Indels 6; Gaps 2;

QY 906 GATGACCAATACAAATAAGAGTTTCCATTTCCATCTGTTATTCACCTGTGACTCATAC 965
DB 43 GCTGACCCAGTACGCGCGAGCATCCGCGCGCTCGCGCTCCCGCGGAGCGCGTGCAC 102
QY 966 TAATGCTGCTGTAATGGCTTGTCTCTCAAGGAGTTACTCAATTTTCACTGTGCGGAAAC 1025
DB 103 CAACGTCCTCGGCGAGTACCTGGCCAAGCATGGCAAGACCCAGCTGCGCATCGCGGAGC 162
QY 1026 TGAGAGTATCCCTCATCTTACCTTCTTCTTAATGTTGGTGGAGAGTTCAATTTCCACGA 1085
DB 163 CGAGAAGTACGCCCATGTGACCTTCTTCTTCGCGCGCGCGCGGAGAACCTTACGAGGG 222
QY 1086 TGAAGAGCTGTGATGGTTCCGTCACCAALAGAAGTTGCTACATATGATTTTAAACACGA 1145
DB 223 CGAGGAGCGCATCTGATCCCTCGCGCA---AGGTGCGCACCTTACCACTGCAACCGCA 279
QY 1146 AATGAATGCTGCTGGAGTTCGCCGAAAAAATGTTGTCAGCAAAATGAGTCAGGACGATCC 1205
DB 280 GATGAGCGCGCGGAACTCACCAGCCGCTATCTGTCGAGGCCATCGAGCAACAGCGCTACGA 339

[illegible][illegible]

Db 98 AAATTGAGCACTTAAATGCCGAATTTGCTACTGTTCAGGCGTCTACTATGCTATGATA 39
QY 605 GGGCAAAAGATGGAGCGCTATTAAAGATGCTTATGA 641
Db 38 GGGATAATCCCTGGATAGGACATGTAAAGCTTATGA 2

RESULT 14
US-09-106-582-34/c
; Sequence 34, Application US/09106582
; Patent No. 6308402
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; THERAPY
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,582
; FILING DATE: 29-JUN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.439C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 484 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Ehrlichia
; US-09-106-582-34

Query Match 4.7%; Score 81.4; DB 4; Length 484;
Best Local Similarity 53.4%; Pred. No. 5.9e-13;
Matches 244; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

QY 185 ATGTCGGATGCGCAGAGGCTTAATGGGAAATTTCTGAAGTTGGACATTTGAATATAGGAG 244
Db 446 ATGTCGGATGCGCTTCAGGTTCAGGTTCAGGAAATTCAGAGTAGGCGACATAAGTATAGGAT 387

QY 245 CTGGAAGAGTATTATCAAGATATTGTTCCGAATTAATTTGGCTGTTCAACGAACAGAT 304
Db 386 GCGGAGGATAGTGTCTTCCAGGATCTTGTGAGAAATTAATCTTGAGATT-----AATGAGG 333

QY 305 TTGTTACAATCTCAGATGTTGCATCAGCTGAGTGCAGAGAGGGAGTGGTCGAT 364
Db 332 TTCAAGAAATCTCAATTTGTTGACTTTGTGCGCATATACAGCGGAAGGGTGGGGTAT 273

QY 365 TGCAATTATTAGGACTGGTTAGCGATGGTGGTGTCCACTCTCATATTGATCATCTTTTGG 424
Db 272 GCCACATGATGGTCTGCTTTCTGATGGTGGAGTGCAATCTCTTCAGGCGCACATGAAA 213

QY 425 CGTTGATACGTGCATTTAAACAATTAACAAGTGCACAAAGGTTTTTCATTCTACTTTTTTGTG 484

Db 212 CCATTAT---TCAGGTTATCACCGGATTTGGCATCAAGGTTTTTATATCATGTAATCTAG 156
QY 485 ATGTCGAGATACCTTCGCCCAACAAGTGGAGCTGTTATCTTGAACAACCTTCTTCAATTTA 544
Db 155 ATGCTAGGATGTT---CCACCCTGCTGCTGCTGAGAAGTATATCGGTATGCTGAACGCTA 99
QY 545 TTGCTTTCGGAAGATACGGAGAAATTTGGCTACTTACTTGACGCTTATTATGCAATGATA 604
Db 98 AAATTGAGCACTTAAATGCCGAATTTGCTACTGTTCAGGCGCTTACTATGCTATGATA 39
QY 605 GGGCAAAAGATGGAGCGCTATTAAAGATGCTTATGA 641
Db 38 GGGATAATCCCTGGATAGGACATGTAAAGCTTATGA 2

RESULT 15
US-09-398-395A-55
; Sequence 55, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
; US-09-398-395A-55

Query Match 2.3%; Score 39.8; DB 4; Length 2861;
Best Local Similarity 53.5%; Pred. No. 0.38;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 1449 AACATTTGTTTTAAATCGACTCCACTACTGAGATGATGGCAAAAGACGTGCACGAGC 1508
Db 2177 AACAGCGTCTCTCATTTAGTGCTCTTTTTCACCTGGGAGGTTCTTTACAGATGAAGTACTCTC 2236

QY 1509 CTTACGTGATGTTCACCGACTGTTCTACAATTAATGGGCTTACCTGTACCGCGCGAGAT 1568
Db 2237 CAAAATTGATCGGATCTAGATTCTTCAACTCATGGCTTAACAGGGCGTTTGGTGAA 2296

QY 1569 GGATGGCGTTCCTTTTACTTTGAACAGAGAGATAAG 1603
Db 2297 TGACACCAAAACTTTATCAGCGCAGAGAGGTCAAG 2331

Search completed: August 4, 2003, 14:22:23
Job time : 97 secs